Analysis of Phylogenetics and Evolution with R (Use R!)

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The increasing availability of molecular and genetic databases coupled with the growing power of computers gives biologists opportunities to address new issues, such as the patterns of molecular evolution, and re-assess old ones, such as the role of adaptation in species diversification.In the second edition, the book continues to integrate a wide variety of data analysis methods into a single and flexible interface: the R language. This open source language is available for a wide range of computer systems and has been adopted as a computational environment by many authors of statistical software. Adopting R as a main tool for phylogenetic analyses will ease the workflow in biologists' data analyses, ensure greater scientific repeatability, and enhance the exchange of ideas and methodological developments. The second edition is completed updated, covering the full gamut of R packages for this area that have been introduced to the market since its previous publication five years ago. There is also a new chapter on the simulation of evolutionary data. Graduate students and researchers in evolutionary biology can use this book as a reference for data analyses, whereas researchers in bioinformatics interested in evolutionary analyses will learn how to implement these methods in R. The book starts with a presentation of different R packages and gives a short introduction to R for phylogeneticists unfamiliar with this language. The basic phylogenetic topics are covered: manipulation of phylogenetic data, phylogeny estimation, tree drawing, phylogenetic comparative methods, and estimation of ancestral characters. The chapter on tree drawing uses R's powerful graphical environment. A section deals with the analysis of diversification with phylogenies, one of the author's favorite research topics. The last chapter is devoted to the development of phylogenetic methods with R and interfaces with otherlanguages (C and C++). Some exercises conclude these chapters.

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